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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/927,738

DATE: 12/20/2001
TIME: 08:55:03

Input Set : A:\initialseq.ST25.txt
Output Set: N:\CRF3\12192001\I927738.raw

3 <110> APPLICANT: Wang, Tongwen
5 <120> TITLE OF INVENTION: Composistions and Methods of modulating TGF-B Signaling
7 <130> FILE REFERENCE: 17633/1082
C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/927,738
10 <141> CURRENT FILING DATE: 2001-08-10
12 <150> PRIOR APPLICATION NUMBER: US 60/119786
13 <151> PRIOR FILING DATE: 1999-02-11
15 <150> PRIOR APPLICATION NUMBER: PCT/US00/03561
16 <151> PRIOR FILING DATE: 2000-02-11
18 <160> NUMBER OF SEQ ID NOS: 28
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 277
24 <212> TYPE: PRT
25 <213> ORGANISM: Unknown
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Isolated using yeast two hybrid system, Clone S1 + 27
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32 Lys Ser Ser Pro Leu Leu Ile Arg Met Glu Glu Ser Leu Asn Ile Val
33 1 5 10 15
36 Lys Tyr Thr Ala Phe Leu Tyr Asn Asp Gln Leu Ile Trp Ser Gly Leu
37 20 25 30
40 Glu Gln Asp Asp Met Arg Ile Leu Tyr Lys Tyr Leu Thr Thr Ser Leu
41 35 40 45
44 Phe Pro Arg His Ile Glu Pro Glu Leu Ala Gly Arg Asp Ser Pro Ile
45 50 55 60
48 Arg Ala Glu Met Pro Gly Asn Leu Gln His Tyr Gly Arg Phe Leu Thr
49 65 70 75 80
52 Gly Pro Leu Asn Leu Asn Asp Pro Asp Ala Lys Cys Arg Phe Pro Lys
53 85 90 95
56 Ile Phe Val Asn Thr Asp Asp Thr Tyr Glu Glu Leu His Leu Ile Val
57 100 105 110
60 Tyr Lys Ala Met Ser Ala Ala Val Cys Phe Met Ile Asp Ala Ser Val
61 115 120 125
64 His Pro Thr Leu Asp Phe Cys Arg Arg Leu Asp Ser Ile Val Gly Pro
65 130 135 140
68 Gln Leu Thr Val Leu Ala Ser Asp Ile Cys Glu Gln Phe Asn Ile Asn
69 145 150 155 160
72 Lys Arg Met Ser Gly Ser Glu Lys Glu Pro Gln Phe Lys Phe Ile Tyr
73 165 170 175
76 Phe Asn His Met Asn Leu Ala Glu Lys Ser Thr Val His Met Arg Lys
77 180 185 190
80 Thr Pro Ser Val Ser Leu Thr Ser Val His Pro Asp Leu Met Lys Ile
81 195 200 205
84 Leu Gly Asp Ile Asn Ser Asp Phe Thr Arg Val Asp Glu Asp Glu Glu
85 210 215 220
88 Ile Ile Val Lys Ala Met Ser Asp Tyr Trp Val Val Gly Lys Lys Ser

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89 225 230 235 240
92 Asp Arg Arg Glu Leu Tyr Val Ile Leu Asn Gln Lys Asn Ala Asn Leu
93 245 250 255
96 Ile Glu Val Asn Glu Val Lys Lys Leu Cys Ala Thr Gln Phe Asn Asn
97 260 265 270
100 Ile Phe Phe Leu Asp
101 275
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 543
106 <212> TYPE: PRT
107 <213> ORGANISM: Unknown
109 <220> FEATURE:
110 <223> OTHER INFORMATION: Clone S1 + 28 protein
112 <400> SEQUENCE: 2
114 Phe Ala Val Asp Ala Lys Ala Leu Pro Gln Asn Lys Pro Arg Pro Leu
115 1 5 10 15
118 Thr Gln Glu Glu Ile Ala Gln Arg Arg Glu Arg Ala Arg Gln Arg His
119 20 25 30
122 Ala Glu Lys Leu Ala Ala Ala Gln Gly Gln Ala Pro Leu Glu Pro Thr
123 35 40 45
126 Gln Asp Gly Ser Ala Ile Glu Thr Cys Pro Lys Gly Asp Glu Pro Arg
127 50 55 60
130 Gly Asp Glu Gln Gln Val Glu Ser Met Thr Pro Lys Pro Val Leu Gln
131 65 70 75 80
134 Glu Glu Asn Asn Gln Glu Ser Phe Ile Ala Phe Ala Arg Val Phe Ser
135 85 90 95
138 Gly Val Ala Arg Arg Gly Lys Lys Ile Phe Val Leu Gly Pro Lys Tyr
139 100 105 110
142 Ser Pro Leu Glu Phe Leu Arg Arg Val Pro Leu Cys Phe Ser Ala Pro
143 115 120 125
146 Pro Asp Gly Leu Pro Gln Val Pro His Met Ala Tyr Cys Ala Leu Glu
147 130 135 140
150 Asn Leu Tyr Leu Leu Met Gly Arg Glu Leu Glu Tyr Leu Glu Glu Val
151 145 150 155 160
154 Pro Pro Gly Asn Val Leu Gly Ile Gly Gly Leu Gln Asp Phe Val Leu
155 165 170 175
158 Lys Ser Ala Thr Leu Cys Ser Leu Pro Ser Cys Pro Pro Phe Ile Pro
159 180 185 190
162 Leu Asn Phe Glu Ala Thr Pro Ile Val Arg Val Ala Val Glu Pro Lys
163 195 200 205
166 His Pro Ser Glu Met Pro Gln Leu Val Lys Gly Met Lys Leu Leu Asn
167 210 215 220
170 Gln Ala Asp Pro Cys Val Gln Ile Leu Ile Gln Glu Thr Gly Glu His
171 225 230 235 240
174 Val Leu Val Thr Ala Gly Glu Val His Leu Gln Arg Cys Leu Asp Asp
175 245 250 255
178 Leu Lys Glu Arg Phe Ala Lys Ile His Ile Ser Val Ser Glu Pro Ile
179 260 265 270
182 Ile Pro Phe Arg Glu Thr Ile Thr Lys Pro Pro Lys Val Asp Met Val

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183 275 280 285
186 Asn Glu Glu Ile Gly Lys Gln Gln Lys Val Ala Val Ile His Gln Met
187 290 295 300
190 Lys Glu Asp Gln Ser Lys Ile Pro Glu Gly Ile Gln Val Asp Ser Asp
191 305 310 315 320
194 Gly Leu Ile Thr Ile Thr Thr Pro Asn Lys Leu Ala Thr Leu Ser Val
195 325 330 335
198 Arg Ala Met Pro Leu Pro Glu Glu Val Thr Gln Ile Leu Glu Glu Asn
199 340 345 350
202 Ser Asp Leu Ile Arg Ser Met Glu Gln Leu Thr Ser Ser Leu Asn Glu
203 355 360 365
206 Gly Glu Asn Thr His Met Ile His Gln Lys Thr Gln Glu Lys Ile Trp
207 370 375 380
210 Glu Phe Lys Gly Lys Leu Glu Gln His Leu Thr Gly Arg Arg Trp Arg
211 385 390 395 400
214 Asn Ile Val Asp Gln Ile Trp Ser Phe Gly Pro Arg Lys Cys Gly Pro
215 405 410 415
218 Asn Ile Leu Val Asn Lys Ser Glu Asp Phe Gln Asn Ser Val Trp Thr
219 420 425 430
222 Gly Pro Ala Asp Lys Ala Ser Lys Glu Ala Ser Arg Tyr Arg Asp Leu
223 435 440 445
226 Gly Asn Ser Ile Val Ser Gly Phe Gln Leu Ala Thr Leu Ser Gly Pro
227 450 455 460
230 Met Cys Glu Glu Pro Leu Met Gly Val Cys Phe Val Leu Glu Lys Trp
231 465 470 475 480
234 Asp Leu Ser Lys Phe Glu Glu Gln Gly Ala Ser Asp Leu Ala Lys Glu
235 485 490 495
238 Asp Arg Arg Lys Met Lys Pro Val Leu Val Glu Met Lys Thr Lys Ser
239 500 505 510
242 Tyr Lys Met Ala Ala Leu Arg Pro Leu Arg Arg Gly His His Arg Lys
243 515 520 525
246 Glu Asn Leu His Ser Leu Thr Ala Met Asp Leu Ser Gln Asp Ser
247 530 535 540

250 <210> SEQ ID NO: 3

251 <211> LENGTH: 396

252 <212> TYPE: PRT

253 <213> ORGANISM: Unknown

255 <220> FEATURE:

256 <223> OTHER INFORMATION: Clone S1 + 19

258 <400> SEQUENCE: 3

260 Met Lys Ala Val Lys Ser Glu Arg Glu Arg Gly Ser Arg Arg Arg His
261 1 5 10 15
264 Arg Asp Gly Asp Val Val Leu Pro Ala Gly Val Val Val Lys Gln Glu
265 20 25 30
268 Arg Leu Ser Pro Glu Val Ala Pro Pro Ala His Arg Arg Pro Asp His
269 35 40 45
272 Ser Gly Gly Ser Pro Ser Pro Pro Thr Ser Glu Pro Ala Arg Ser Gly
273 50 55 60
276 His Arg Gly Asn Arg Ala Arg Gly Val Ser Arg Ser Pro Pro Lys Lys

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277 65 70 75 80
280 Lys Asn Lys Ala Ser Gly Arg Arg Ser Lys Ser Pro Arg Ser Lys Arg
281 85 90 95
284 Asn Arg Ser Pro His His Ser Thr Val Lys Val Lys Gln Glu Arg Glu
285 100 105 110
288 Asp His Pro Arg Arg Gly Arg Glu Asp Arg Gln His Arg Glu Pro Ser
289 115 120 125
292 Glu Gln Glu His Arg Arg Ala Arg Asn Ser Asp Arg Asp Arg His Arg
293 130 135 140
296 Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro Gly Ser Gly
297 145 150 155 160
300 Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln Ala Gln Glu
301 165 170 175
304 Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His Arg Gln Arg
305 180 185 190
308 Asn Asp Val Gly Gly Gly Ser Glu Ser Gln Glu Leu Val Pro Arg
309 195 200 205
312 Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys Glu Lys Pro
313 210 215 220
316 Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn Thr Phe Arg
317 225 230 235 240
320 Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg Ile Pro Lys
321 245 250 255
324 Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val Leu Pro Val
325 260 265 270
328 Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg His Arg Arg
329 275 280 285
332 Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys Gln His Ala
333 290 295 300
336 Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp Gly Thr Val
337 305 310 315 320
340 Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser Gly Asn Gly
341 325 330 335
344 Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr Tyr Glu Leu
345 340 345 350
348 Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg Glu Tyr Val
349 355 360 365
352 Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg Lys Asp Asp
353 370 375 380
356 Glu Asp Glu Glu Glu Glu Val Ser Asp Ser
357 385 390 395
360 <210> SEQ ID NO.: 4
361 <211> LENGTH: 82
362 <212> TYPE: PRT
363 <213> ORGANISM: Unknown
365 <220> FEATURE:
366 <223> OTHER INFORMATION: Protein Sequence of NIPP-1 domain homologous to SNIP 1
368 <400> SEQUENCE: 4
370 Tyr Leu Phe Gly Arg Asn Pro Asp Leu Cys Asp Phe Thr Ile Asp His

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371 1      5      10      15
374 Gln Ser Cys Ser Arg Val His Ala Ala Leu Val Tyr His Lys His Leu
375          20      25      30
378 Lys Arg Val Phe Leu Ile Asp Leu Asn Ser Thr His Gly Thr Phe Leu
379          35      40      45
382 Gly His Ile Arg Leu Glu Pro His Lys Pro Gln Gln Ile Pro Ile Asp
383          50      55      60
386 Ser Thr Val Ser Phe Gly Ala Ser Thr Arg Ala Tyr Thr Leu Arg Glu
387 65      70      75      80
390 Lys Pro
394 <210> SEQ ID NO: 5
395 <211> LENGTH: 255
396 <212> TYPE: PRT
397 <213> ORGANISM: Unknown
399 <220> FEATURE:
400 <223> OTHER INFORMATION: Clone S1 + 19 Smad binding domain sequence
402 <400> SEQUENCE: 5
404 Arg His Arg Gly His Ser His Gln Arg Arg Thr Ser Asn Glu Arg Pro
405 1      5      10      15
408 Gly Ser Gly Gln Gly Gln Gly Arg Asp Arg Asp Thr Gln Asn Leu Gln
409          20      25      30
412 Ala Gln Glu Glu Glu Arg Glu Phe Tyr Asn Ala Arg Arg Arg Glu His
413          35      40      45
416 Arg Gln Arg Asn Asp Val Gly Gly Gly Ser Glu Ser Gln Glu Leu
417          50      55      60
420 Val Pro Arg Pro Gly Gly Asn Asn Lys Glu Lys Glu Val Pro Ala Lys
421 65      70      75      80
424 Glu Lys Pro Ser Phe Glu Leu Ser Gly Ala Leu Leu Glu Asp Thr Asn
425          85      90      95
428 Thr Phe Arg Gly Val Val Ile Lys Tyr Ser Glu Pro Pro Glu Ala Arg
429          100     105     110
432 Ile Pro Lys Lys Arg Trp Arg Leu Tyr Pro Phe Lys Asn Asp Glu Val
433          115     120     125
436 Leu Pro Val Met Tyr Ile His Arg Gln Ser Ala Tyr Leu Leu Gly Arg
437          130     135     140
440 His Arg Arg Ile Ala Asp Ile Pro Ile Asp His Pro Ser Cys Ser Lys
441 145     150     155     160
444 Gln His Ala Val Phe Gln Tyr Arg Leu Val Glu Tyr Thr Arg Ala Asp
445          165     170     175
448 Gly Thr Val Gly Arg Arg Val Lys Pro Tyr Ile Ile Asp Leu Gly Ser
449          180     185     190
452 Gly Asn Gly Thr Phe Leu Asn Asn Lys Arg Ile Glu Pro Gln Arg Tyr
453          195     200     205
456 Tyr Glu Leu Lys Glu Lys Asp Val Leu Lys Phe Gly Phe Ser Ser Arg
457          210     215     220
460 Glu Tyr Val Leu Leu His Glu Ser Ser Asp Thr Ser Glu Ile Asp Arg
461 225     230     235     240
464 Lys Asp Asp Glu Asp Glu Glu Glu Glu Val Ser Asp Ser
465          245     250     255

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Use of n and/or Xaa has been detected in the Sequence Listing.

Review the Sequence Listing to insure a corresponding

explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/927,738

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Input Set : A:\initialseq.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10

L:931 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11

L:1240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16